Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:08:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231735.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6231735 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231735.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:08:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231735.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,296,559
Mapped reads	4,939,077 / 93.25%
Unmapped reads	357,482 / 6.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,630 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	467,403 / 8.82%
Duplication rate	4.09%
Clipped reads	1,973,421 / 37.26%

2.2. ACGT Content

Number/percentage of A's	89,330,091 / 26.66%
Number/percentage of C's	61,830,941 / 18.46%
Number/percentage of T's	97,221,529 / 29.02%
Number/percentage of G's	86,566,289 / 25.84%
Number/percentage of N's	74,078 / 0.02%
GC Percentage	44.29%

2.3. Coverage

Mean	0.1083

Standard Deviation	30.0757

2.4. Mapping Quality

Mean Mapping Quality	45.3

2.5. Mismatches and indels

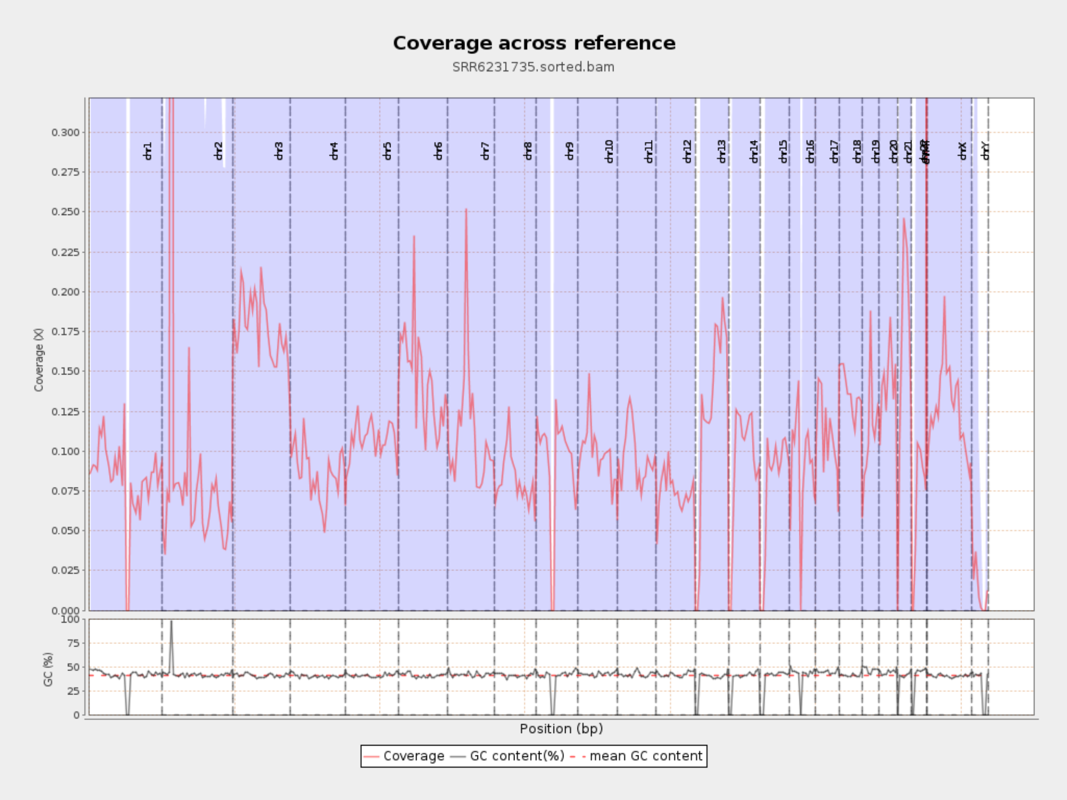
General error rate	0.67%
Mismatches	2,214,522
Insertions	23,342
Mapped reads with at least one insertion	0.47%
Deletions	77,595
Mapped reads with at least one deletion	1.56%
Homopolymer indels	46.61%

2.6. Chromosome stats

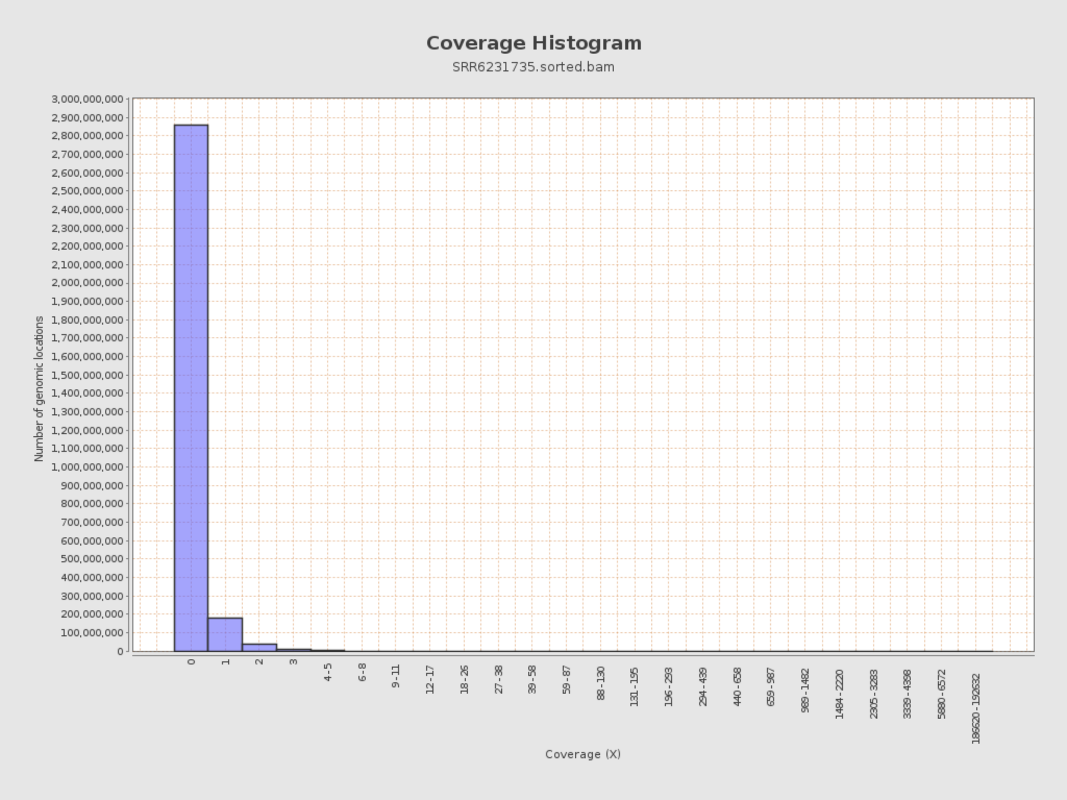
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20565654	0.0825	1.3367
chr2	243199373	31832092	0.1309	107.2629
chr3	198022430	35170494	0.1776	0.5485
chr4	191154276	16437252	0.086	0.4166
chr5	180915260	19512954	0.1079	0.432
chr6	171115067	24690405	0.1443	0.7516
chr7	159138663	17900499	0.1125	1.8095

chr8	146364022	12000867	0.082	1.0928
chr9	141213431	13002859	0.0921	0.7627
chr10	135534747	13425923	0.0991	0.7493
chr11	135006516	12914712	0.0957	0.9598
chr12	133851895	9851469	0.0736	0.3853
chr13	115169878	14574628	0.1265	0.4622
chr14	107349540	9873019	0.092	0.5305
chr15	102531392	8090096	0.0789	0.3591
chr16	90354753	8343302	0.0923	0.4572
chr17	81195210	8884869	0.1094	0.5605
chr18	78077248	10693819	0.137	1.4675
chr19	59128983	6774443	0.1146	0.9958
chr20	63025520	8949597	0.142	0.5227
chr21	48129895	7894017	0.164	0.5858
chr22	51304566	3375412	0.0658	0.3247
chrMT	16571	12084	0.7292	1.1399
chrX	155270560	19567543	0.126	0.5896
chrY	59373566	810808	0.0137	0.2299

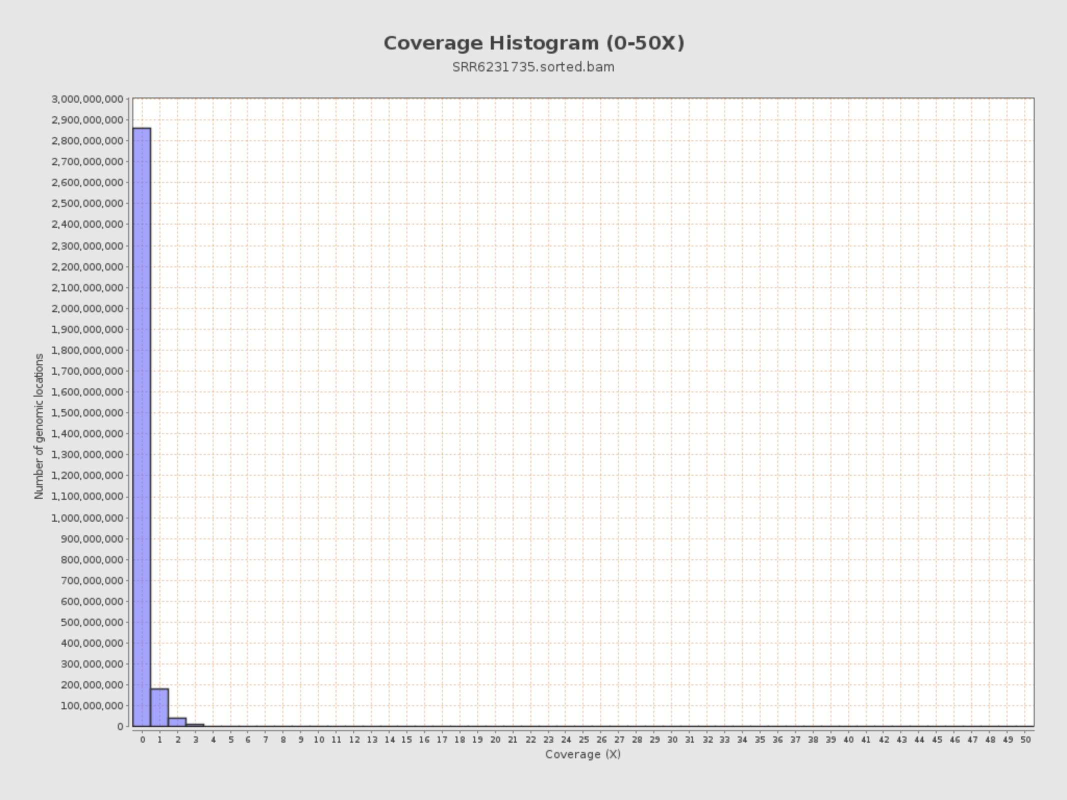
3. Results : Coverage across reference



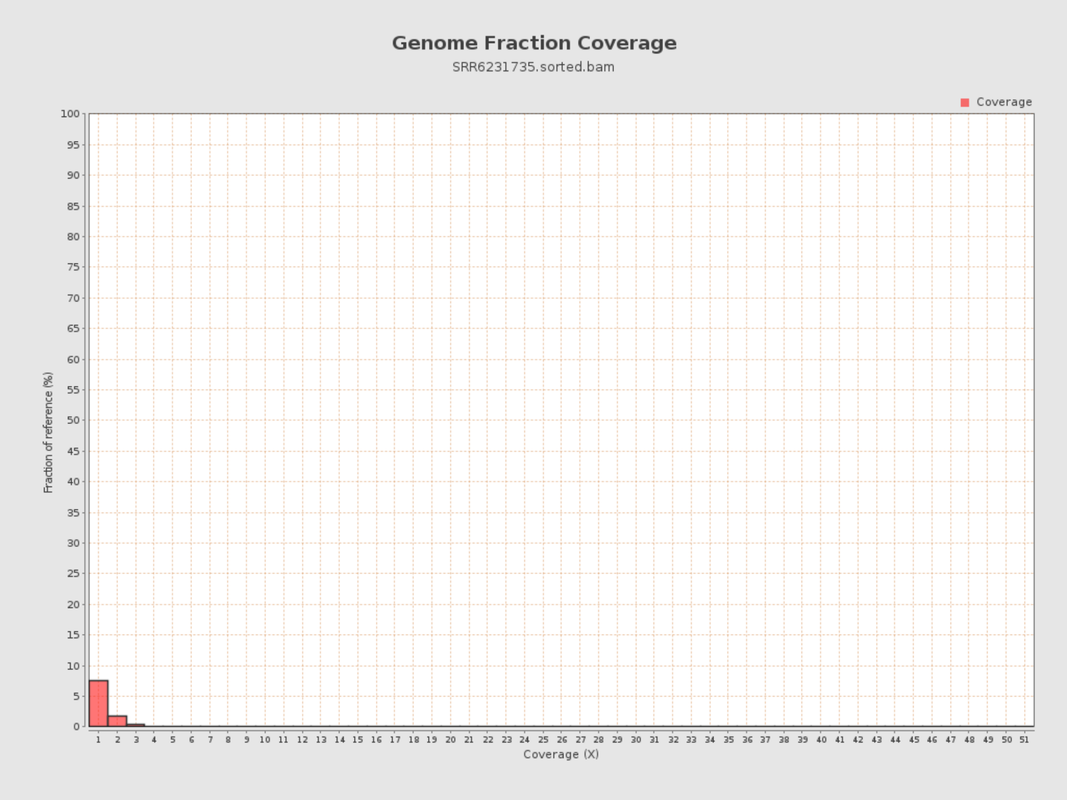
4. Results : Coverage Histogram



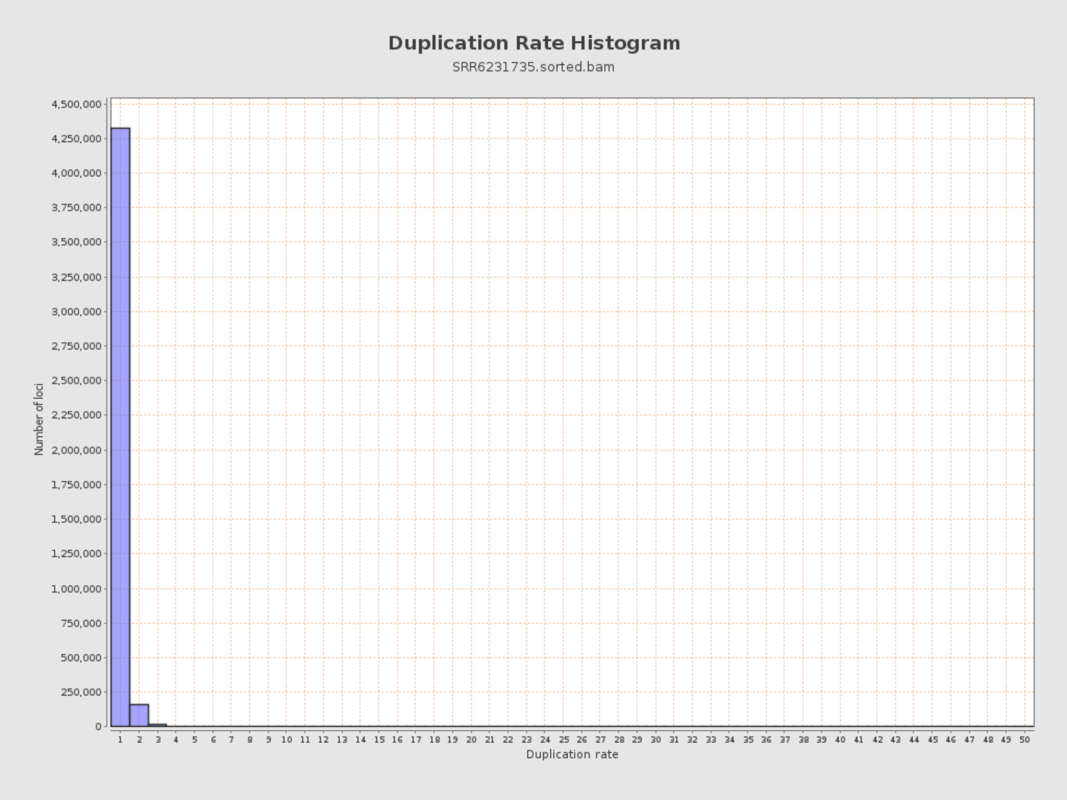
5. Results : Coverage Histogram (0-50X)



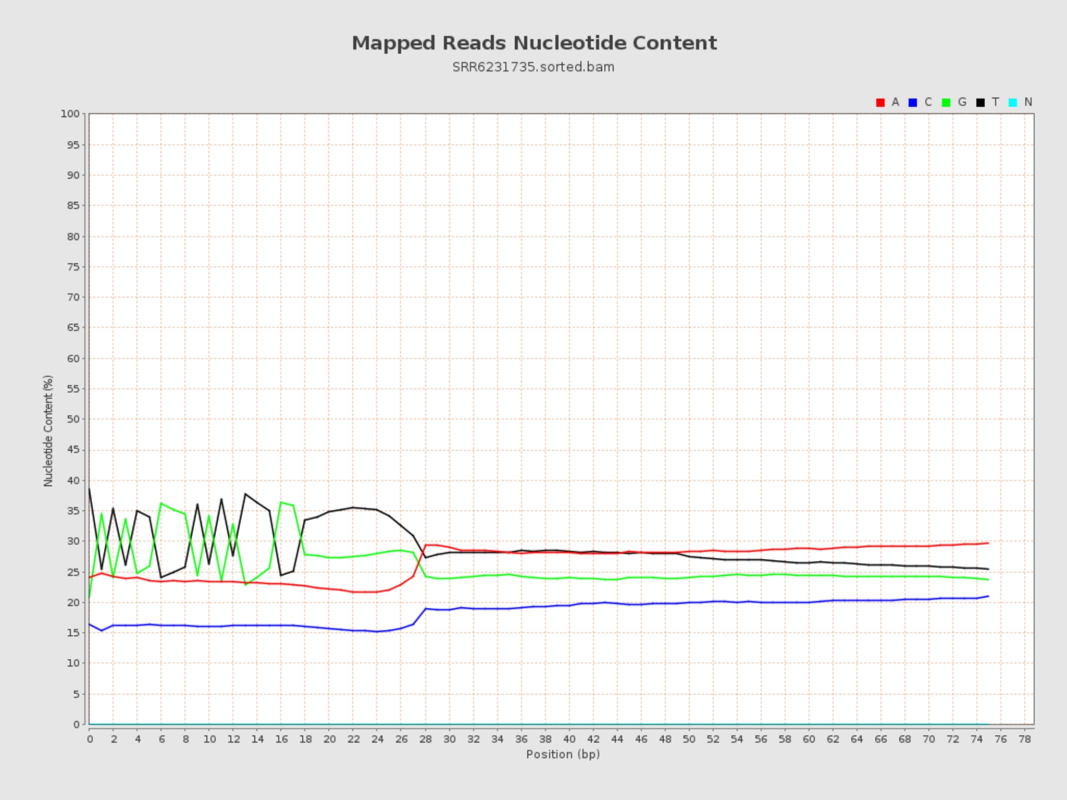
6. Results : Genome Fraction Coverage



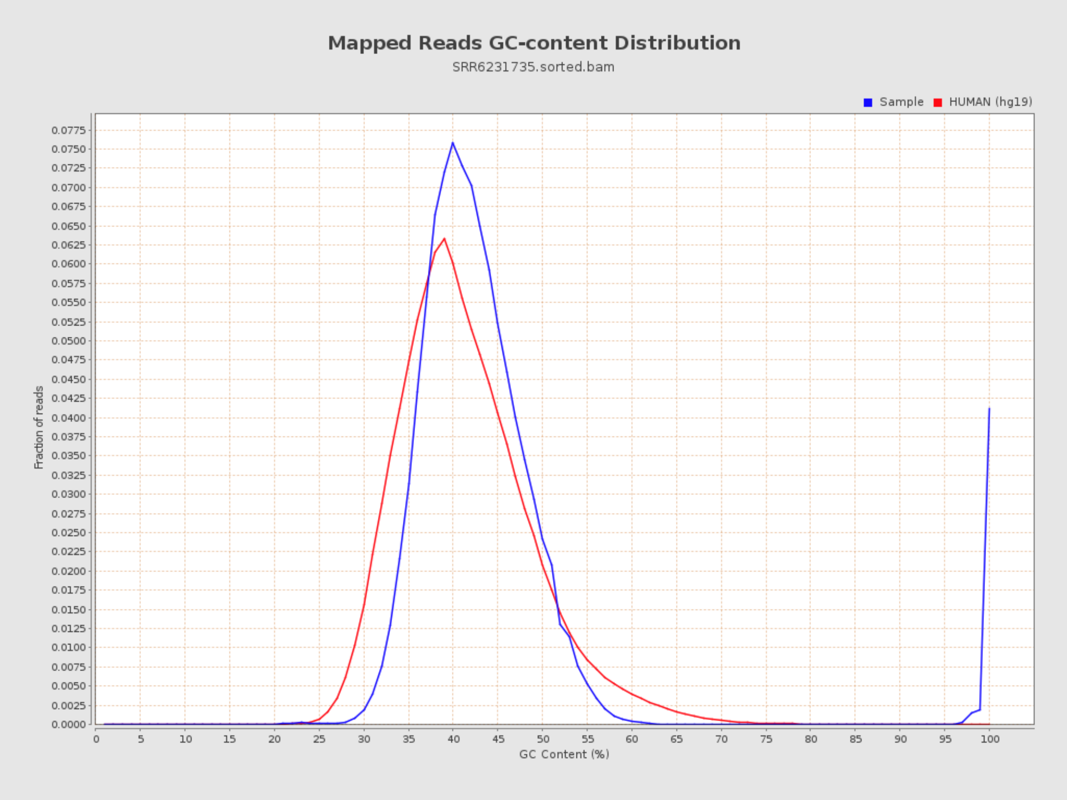
7. Results : Duplication Rate Histogram



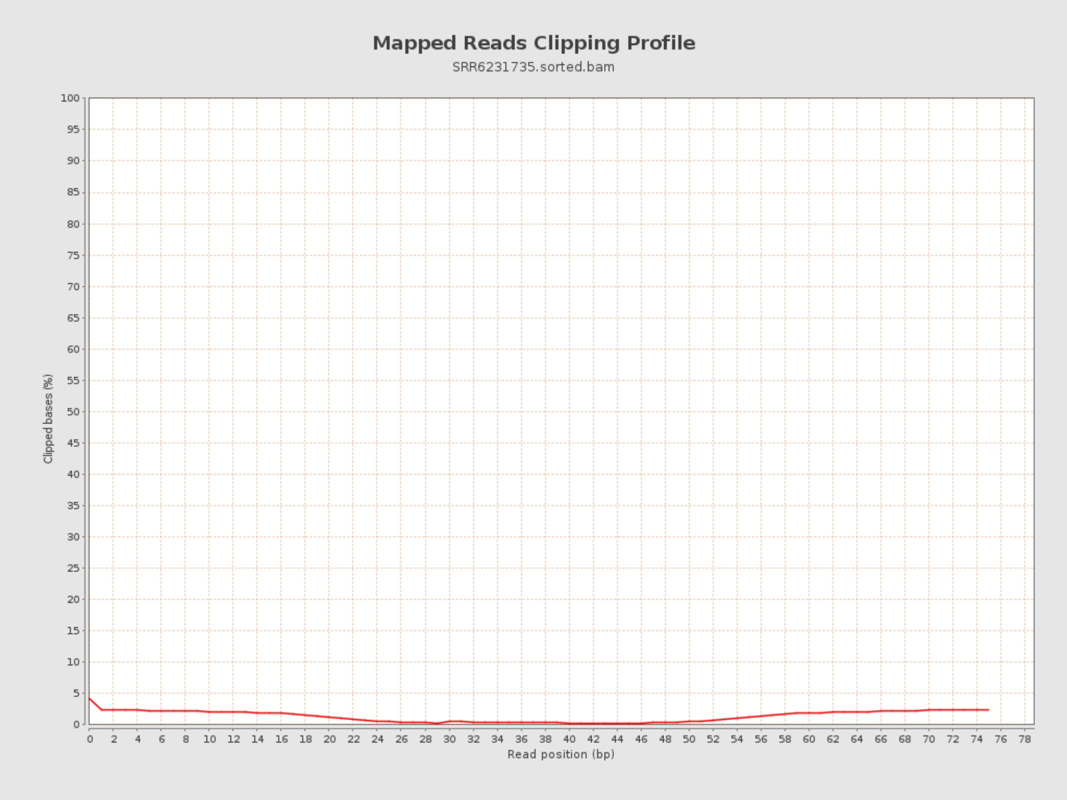
8. Results : Mapped Reads Nucleotide Content



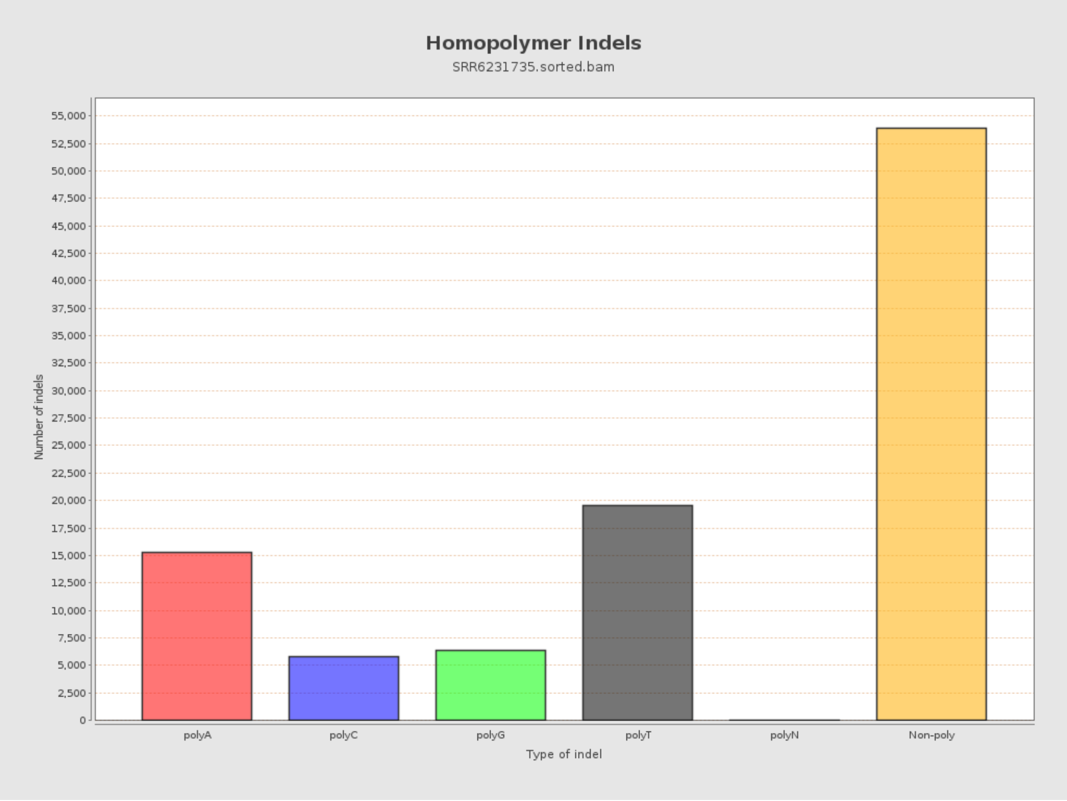
9. Results : Mapped Reads GC-content Distribution



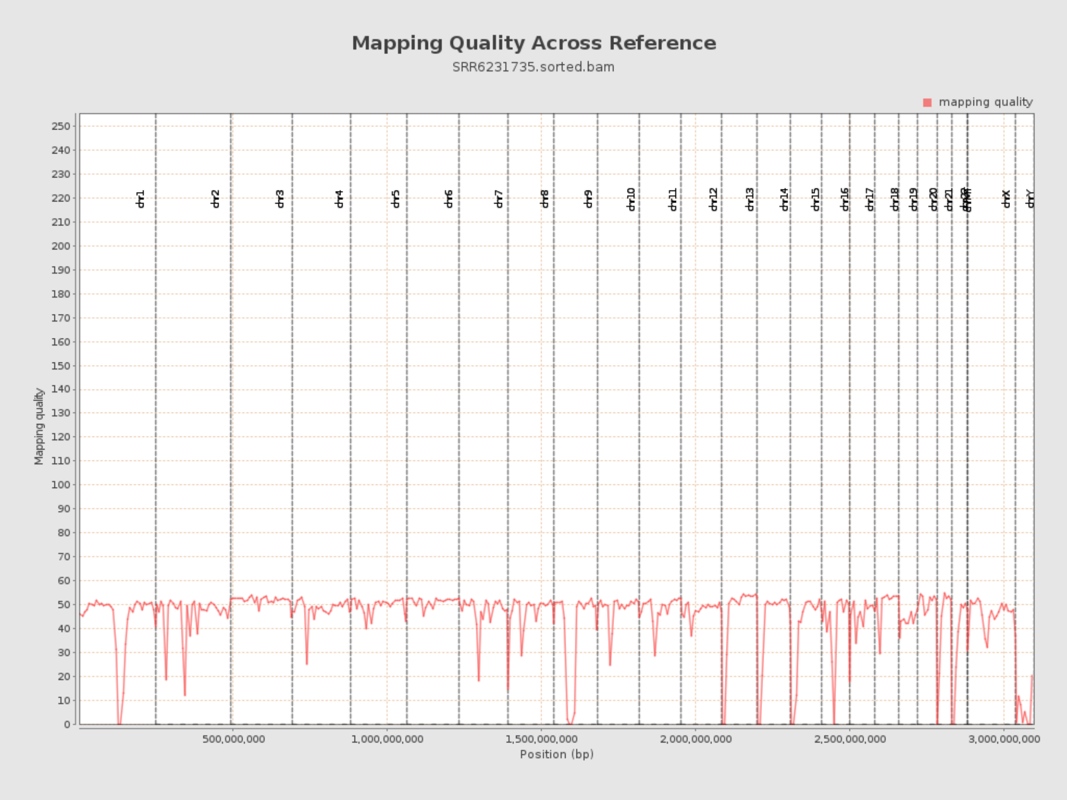
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram